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TECH CENTER 1600/2900

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Freyssinet, Georges
Perez, Pascal

<120> METHOD FOR OBTAINING PLANT VARIETIES

<130> A33153-PCT-USA 072667.0128

<140> US 09/529,239

<141> 2000-10-27

<150> PCT/EP98/06977

<151> 1998-10-09

<160> 98

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<223> Degenerate oligonucleotides UPMU used to isolate AtMSH3 and AtMSH6.

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<301> Reenan and Kolodner

<302> Genetics

<303> 132

<306> 963,973

<307> 1992

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 <223> Primer AP1 for PCR using cDNA of Arabidopsis thaliana ecotype Columbia containing adapter sequences ligated to both its ends

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 <210> 5
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Columbia
containing adapter sequences ligated to both its ends

<400> 5

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<211> 30

<212> DNA

<213> Artificial sequence

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<223> MSH3 specific primer S525 for PCR using cDNA of Arabidopsis
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<210> 7

<211> 29

<212> DNA

<213> Artificial sequence

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<223> MSH3 specific primer S51 for PCR using cDNA of Arabidopsis
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<210> 8

<211> 24

<212> DNA

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<210> 9

<211> 28

<212> DNA

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ecotype Columbia

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<212> DNA

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ecotype Columbia

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<212> DNA

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360

ccagatgtgg ttttgatggt ggaagtgggt tacaggtaca gattcttcgg agaagacgcg

420

gagatcgcag cagcgtgtt gggatattac gctcatatgg atcacaattt catgacggcg

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<210> 14
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 <212> DNA
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ttgacccggg 2110

<210> 16
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<212> DNA
<213> Artificial sequence

<220>
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ecotype Columbia

<400> 16
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<210> 17
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> MSH3 specific primer S525 for PCR using cDNA of Arabidopsis
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ecotype Columbia

<400> 17
aggttctgat tatgtgtgac gctttactta 30

<210> 18
<211> 3522
<212> DNA
<213> Arabidopsis thaliana ecotype Columbia

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<221> CDS
<222> (100)...(3342)
<223> AtMSH3 full-length cDNA and deduced sequence of the encoded
polypeptide

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catttctctt aaacggagga gattacgaat aaagcaatt 99
atg ggc aag caa aag cag cag acg att tct cgt ttc ttc gct ccc aaa 147

Met	Gly	Lys	Gln	Lys	Gln	Gln	Thr	Ile	Ser	Arg	Phe	Phe	Ala	Pro	Lys	
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ccc	aaa	tcc	ccg	act	cac	gaa	ccg	aat	ccg	gta	gcc	gaa	tca	tca	aca	195
Pro	Lys	Ser	Pro	Thr	His	Glu	Pro	Asn	Pro	Val	Ala	Glu	Ser	Ser	Thr	
			20					25					30			
ccg	cca	ccg	aag	ata	tcc	gcc	act	gta	tcc	ttc	tct	cct	tcc	aag	cgt	243
Pro	Pro	Pro	Lys	Ile	Ser	Ala	Thr	Val	Ser	Phe	Ser	Pro	Ser	Lys	Arg	
			35				40					45				
aag	ctt	ctc	tcc	gac	cac	ctc	gcc	gcc	gcg	tca	ccc	aaa	aag	cct	aaa	291
Lys	Leu	Leu	Ser	Asp	His	Leu	Ala	Ala	Ala	Ser	Pro	Lys	Lys	Pro	Lys	
	50					55					60					
ctt	tct	cct	cac	act	caa	aac	cca	gta	ccc	gat	ccc	aat	tta	cac	caa	339
Leu	Ser	Pro	His	Thr	Gln	Asn	Pro	Val	Pro	Asp	Pro	Asn	Leu	His	Gln	
	65				70					75					80	
aga	ttt	ctc	cag	aga	ttt	ctg	gaa	ccc	tcg	ccg	gag	gaa	tat	gtt	ccc	387
Arg	Phe	Leu	Gln	Arg	Phe	Leu	Glu	Pro	Ser	Pro	Glu	Glu	Tyr	Val	Pro	
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gaa	acg	tca	tca	tcg	agg	aaa	tac	aca	cca	ttg	gaa	cag	caa	gtg	gtg	435
Glu	Thr	Ser	Ser	Ser	Arg	Lys	Tyr	Thr	Pro	Leu	Glu	Gln	Gln	Val	Val	
			100					105					110			
gag	cta	aag	agc	aag	tac	cca	gat	gtg	gtt	ttg	atg	gtg	gaa	gtt	ggt	483
Glu	Leu	Lys	Ser	Lys	Tyr	Pro	Asp	Val	Val	Leu	Met	Val	Glu	Val	Gly	
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tac	agg	tac	aga	ttc	ttc	gga	gaa	gac	gcg	gag	atc	gca	gca	cgc	gtg	531
Tyr	Arg	Tyr	Arg	Phe	Phe	Gly	Glu	Asp	Ala	Glu	Ile	Ala	Ala	Arg	Val	
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Leu	Gly	Ile	Tyr	Ala	His	Met	Asp	His	Asn	Phe	Met	Thr	Ala	Ser	Val	
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cca	aca	ttt	cga	ttg	aat	ttc	cat	gtg	aga	aga	ctg	gtg	aat	gca	gga	627
Pro	Thr	Phe	Arg	Leu	Asn	Phe	His	Val	Arg	Arg	Leu	Val	Asn	Ala	Gly	
				165				170					175			
tac	aag	att	ggt	gta	gtg	aag	cag	act	gaa	act	gca	gcc	att	aag	tcc	675
Tyr	Lys	Ile	Gly	Val	Val	Lys	Gln	Thr	Glu	Thr	Ala	Ala	Ile	Lys	Ser	
			180					185					190			
cat	ggt	gca	aac	cgg	acc	ggc	cct	ttt	ttc	cgg	gga	ctg	tcg	gcg	ttg	723
His	Gly	Ala	Asn	Arg	Thr	Gly	Pro	Phe	Phe	Arg	Gly	Leu	Ser	Ala	Leu	
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Tyr	Thr	Lys	Ala	Thr	Leu	Glu	Ala	Ala	Glu	Asp	Ile	Ser	Gly	Gly	Cys	
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ggt	ggt	gaa	gaa	ggt	ttt	ggt	tca	cag	agt	aat	ttc	ttg	gtt	tgt	gtt	819
Gly	Gly	Glu	Glu	Gly	Phe	Gly	Ser	Gln	Ser	Asn	Phe	Leu	Val	Cys	Val	
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gtg	gat	gag	aga	gtt	aag	tcg	gag	aca	tta	ggc	tgt	ggt	att	gaa	atg	867
Val	Asp	Glu	Arg	Val	Lys	Ser	Glu	Thr	Leu	Gly	Cys	Gly	Ile	Glu	Met	

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agt	ttt	gat	gtt	aga	gtc	ggg	gtt	gtt	ggc	gtt	gaa	att	tcg	aca	ggg	915			
Ser	Phe	Asp	Val	Arg	Val	Gly	Val	Val	Gly	Val	Glu	Ile	Ser	Thr	Gly				
260				265				270											
gaa	gtt	gtt	tat	gaa	gag	ttc	aat	gat	aat	ttc	atg	aga	agt	gga	tta	963			
Glu	Val	Val	Tyr	Glu	Glu	Phe	Asn	Asp	Asn	Phe	Met	Arg	Ser	Gly	Leu				
275				280				285											
gag	gct	gtg	att	ttg	agc	ttg	tca	cca	gct	gag	ctg	ttg	ctt	ggc	cag	1011			
Glu	Ala	Val	Ile	Leu	Ser	Leu	Ser	Pro	Ala	Glu	Leu	Leu	Leu	Gly	Gln				
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cct	ctt	tca	caa	caa	act	gag	aag	ttt	ttg	gtg	gca	cat	gct	gga	cct	1059			
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acc	tca	aac	gtt	cga	gtg	gaa	cgt	gcc	tca	ctg	gat	tgt	ttc	agc	aat	1107			
Thr	Ser	Asn	Val	Arg	Val	Glu	Arg	Ala	Ser	Leu	Asp	Cys	Phe	Ser	Asn				
325				330				335				340							
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Gly	Asn	Ala	Val	Asp	Glu	Val	Ile	Ser	Leu	Cys	Glu	Lys	Ile	Ser	Ala				
340				345				350											
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Gly	Asn	Leu	Glu	Asp	Asp	Lys	Glu	Met	Lys	Leu	Glu	Ala	Ala	Glu	Lys				
355				360				365											
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Gly	Met	Ser	Cys	Leu	Thr	Val	His	Thr	Ile	Met	Asn	Met	Pro	His	Leu				
370				375				380											
act	gtt	caa	gcc	ctc	gcc	cta	acg	ttt	tgc	cat	ctc	aaa	cag	ttt	gga	1299			
Thr	Val	Gln	Ala	Leu	Ala	Leu	Thr	Phe	Cys	His	Leu	Lys	Gln	Phe	Gly				
385				390				395				400							
ttt	gaa	agg	atc	ctt	tac	caa	ggg	gcc	tca	ttt	cgc	tct	ttg	tca	agt	1347			
Phe	Glu	Arg	Ile	Leu	Tyr	Gln	Gly	Ala	Ser	Phe	Arg	Ser	Leu	Ser	Ser				
405				410				415											
aac	aca	gag	atg	act	ctc	tca	gcc	aat	act	ctg	caa	cag	ttg	gag	gtt	1395			
Asn	Thr	Glu	Met	Thr	Leu	Ser	Ala	Asn	Thr	Leu	Gln	Gln	Leu	Glu	Val				
420				425				430											
gtg	aaa	aat	aat	tca	gat	gga	tcg	gaa	tct	ggc	tcc	tta	ttc	cat	aat	1443			
Val	Lys	Asn	Asn	Ser	Asp	Gly	Ser	Glu	Ser	Gly	Ser	Leu	Phe	His	Asn				
435				440				445											
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Met	Asn	His	Thr	Leu	Thr	Val	Tyr	Gly	Ser	Arg	Leu	Leu	Arg	His	Trp				
450				455				460											
gtg	act	cat	cct	cta	tgc	gat	aga	aat	ttg	ata	tct	gct	cgg	ctt	gat	1539			
Val	Thr	His	Pro	Leu	Cys	Asp	Arg	Asn	Leu	Ile	Ser	Ala	Arg	Leu	Asp				
465				470				475				480							
gct	gtt	tct	gag	att	tct	gct	tgc	atg	gga	tct	cat	agt	tct	tcc	cag	1587			
Ala	Val	Ser	Glu	Ile	Ser	Ala	Cys	Met	Gly	Ser	His	Ser	Ser	Ser	Gln				
485				490				495											

ctc	agc	agt	gag	ttg	gtt	gaa	gaa	ggt	tct	gag	aga	gca	att	gta	tca	1635
Leu	Ser	Ser	Glu	Leu	Val	Glu	Glu	Gly	Ser	Glu	Arg	Ala	Ile	Val	Ser	
			500					505					510			
cct	gag	ttt	tat	ctc	gtg	ctc	tcc	tca	gtc	ttg	aca	gct	atg	tct	aga	1683
Pro	Glu	Phe	Tyr	Leu	Val	Leu	Ser	Ser	Val	Leu	Thr	Ala	Met	Ser	Arg	
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tca	tct	gat	att	caa	cgt	gga	ata	aca	aga	atc	ttt	cat	cgg	act	gct	1731
Ser	Ser	Asp	Ile	Gln	Arg	Gly	Ile	Thr	Arg	Ile	Phe	His	Arg	Thr	Ala	
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aaa	gcc	aca	gag	ttc	att	gca	gtt	atg	gaa	gct	att	tta	ctt	gcg	ggg	1779
Lys	Ala	Thr	Glu	Phe	Ile	Ala	Val	Met	Glu	Ala	Ile	Leu	Leu	Ala	Gly	
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atg	caa	tct	gca	act	gtg	cga	tct	act	ctt	ttg	aga	aaa	ttg	att	tct	1875
Met	Gln	Ser	Ala	Thr	Val	Arg	Ser	Thr	Leu	Leu	Arg	Lys	Leu	Ile	Ser	
			580					585					590			
gtt	att	tca	tcc	cct	gtt	gtg	gtt	gac	aat	gcc	gga	aaa	ctt	ctc	tct	1923
Val	Ile	Ser	Ser	Pro	Val	Val	Val	Asp	Asn	Ala	Gly	Lys	Leu	Leu	Ser	
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gcc	cta	aat	aag	gaa	gcg	gct	gtt	cga	ggt	gac	ttg	ctc	gac	ata	cta	1971
Ala	Leu	Asn	Lys	Glu	Ala	Ala	Val	Arg	Gly	Asp	Leu	Leu	Asp	Ile	Leu	
	610					615					620					
atc	act	tcc	agc	gac	caa	ttt	cct	gag	ctt	gct	gaa	gct	cgc	caa	gca	2019
Ile	Thr	Ser	Ser	Asp	Gln	Phe	Pro	Glu	Leu	Ala	Glu	Ala	Arg	Gln	Ala	
625					630					635					640	
gtt	tta	gtc	atc	agg	gaa	aag	ctg	gat	tcc	tcg	ata	gct	tca	ttt	cgc	2067
Val	Leu	Val	Ile	Arg	Glu	Lys	Leu	Asp	Ser	Ser	Ile	Ala	Ser	Phe	Arg	
			645					650						655		
aag	aag	ctc	gct	att	cga	aat	ttg	gaa	ttt	ctt	caa	gtg	tcg	ggg	atc	2115
Lys	Lys	Leu	Ala	Ile	Arg	Asn	Leu	Glu	Phe	Leu	Gln	Val	Ser	Gly	Ile	
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Cys Leu His Ser Leu Ser Thr Leu Ser Arg Asn Lys Asn Tyr Val Arg	
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ccc gag ttt gtg gat gac tgt gaa cca gtt gag ata aac ata cag tct	2451
Pro Glu Phe Val Asp Asp Cys Glu Pro Val Glu Ile Asn Ile Gln Ser	
770 775 780	
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Gly Arg His Pro Val Leu Glu Thr Ile Leu Gln Asp Asn Phe Val Pro	
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Gly Pro Asn Met Gly Gly Lys Ser Cys Tyr Ile Arg Gln Val Ala Leu	
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Gly Ser Tyr Asp His Asp Asp Val Thr Tyr Leu Tyr Lys Leu Val Arg	
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 Glu Thr Ser Ser Ser Arg Lys Tyr Thr Pro Leu Glu Gln Gln Val Val

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 485 490 495
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 675 680 685
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 740 745 750

Cys Leu His Ser Leu Ser Thr Leu Ser Arg Asn Lys Asn Tyr Val Arg
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 Phe Gln Lys Pro Thr Ala Ala Thr Thr Lys Gly Leu Val Ser Gly Asp
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 Ala Ala Ser Gly Gly Gly Gly Ser Gly Gly Pro Arg Phe Asn Val Arg
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gaa ggc gat gct aaa ggc gac gct tct gta cgt ttt gct gtt tcg aaa 315
 Glu Gly Asp Ala Lys Gly Asp Ala Ser Val Arg Phe Ala Val Ser Lys
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 Ser Val Asp Glu Val Arg Gly Thr Asp Thr Pro Pro Glu Lys Val Pro
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 Arg Arg Val Leu Pro Ser Gly Phe Lys Pro Ala Glu Ser Ala Gly Asp
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Arg	Ser	Asn	Asn	Gly	Lys	Thr	Gln	Glu	Arg	Asn	His	Ala	Phe	Ser	Phe	
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Ser	Gly	Arg	Ala	Glu	Leu	Arg	Ser	Val	Glu	Asp	Ile	Gly	Val	Asp	Gly	
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gat	ggt	cct	ggg	cca	gaa	aca	cca	ggg	atg	cgt	cca	cgt	gct	tct	cgc	699
Asp	Val	Pro	Gly	Pro	Glu	Thr	Pro	Gly	Met	Arg	Pro	Arg	Ala	Ser	Arg	
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Leu	Lys	Arg	Val	Leu	Glu	Asp	Glu	Met	Thr	Phe	Lys	Glu	Asp	Lys	Val	
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Pro	Val	Leu	Asp	Ser	Asn	Lys	Arg	Leu	Lys	Met	Leu	Gln	Asp	Pro	Val	
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Cys	Gly	Glu	Lys	Lys	Glu	Val	Asn	Glu	Gly	Thr	Lys	Phe	Glu	Trp	Leu	
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Glu	Ser	Ser	Arg	Ile	Arg	Asp	Ala	Asn	Arg	Arg	Arg	Pro	Asp	Asp	Pro	
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Met	Ser	Ala	Ser	Gln	Lys	Gln	Tyr	Trp	Ser	Val	Lys	Ser	Glu	Tyr	Met	
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Ser	Gly	Val	Gly	Lys	Cys	Arg	Gln	Val	Gly	Ile	Ser	Glu	Ser	Gly	Ile	
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gat	gag	gca	gtg	caa	aag	cta	tta	gct	cgt	gga	tat	aaa	ggt	gga	cga	1179
Asp	Glu	Ala	Val	Gln	Lys	Leu	Leu	Ala	Arg	Gly	Tyr	Lys	Val	Gly	Arg	
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Thr Ile Ile Pro Arg Lys Leu Val Gln Val Leu Thr Pro Ser Thr Ala	
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agc gag gga aac atc ggg cct gat gcc gtc cat ctt ctt gct ata aaa	1323
Ser Glu Gly Asn Ile Gly Pro Asp Ala Val His Leu Leu Ala Ile Lys	
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gag atc aaa atg gag cta caa aag tgt tca act gtg tat gga ttt gct	1371
Glu Ile Lys Met Glu Leu Gln Lys Cys Ser Thr Val Tyr Gly Phe Ala	
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Phe Val Asp Cys Ala Ala Leu Arg Phe Trp Val Gly Ser Ile Ser Asp	
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Asp Ala Ser Cys Ala Ala Leu Gly Ala Leu Leu Met Gln Val Ser Pro	
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Lys Glu Val Leu Tyr Asp Ser Lys Gly Leu Ser Arg Glu Ala Gln Lys	
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Ala Leu Arg Lys Tyr Thr Leu Thr Gly Ser Thr Ala Val Gln Leu Ala	
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Pro Val Pro Gln Val Met Gly Asp Thr Asp Ala Ala Gly Val Arg Asn	
475 480 485 490	
ata ata gaa tct aac gga tac ttt aaa ggt tct tct gaa tca tgg aac	1659
Ile Ile Glu Ser Asn Gly Tyr Phe Lys Gly Ser Ser Glu Ser Trp Asn	
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Cys Ala Val Asp Gly Leu Asn Glu Cys Asp Val Ala Leu Ser Ala Leu	
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Gly Glu Leu Ile Asn His Leu Ser Arg Leu Lys Leu Glu Asp Val Leu	
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Lys His Gly Asp Ile Phe Pro Tyr Gln Val Tyr Arg Gly Cys Leu Arg	
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Ile Asp Gly Gln Thr Met Val Asn Leu Glu Ile Phe Asn Asn Ser Cys	
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Asp Gly Gly Pro Ser Gly Thr Leu Tyr Lys Tyr Leu Asp Asn Cys Val	
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Gln	Arg	Val	Lys	Ala	Phe	Gly	Gln	Ile	Val	Lys	Gly	Phe	Arg	Ser	Gly		
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Ile	Asp	Leu	Leu	Leu	Ala	Leu	Gln	Lys	Glu	Ser	Asn	Met	Met	Ser	Leu		
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gca	agt	ctc	tct	gct	gga	agc	atg	gcc	agg	cct	ggt	att	ttt	ccc	gaa	2523	
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Pro	Val	Pro	Asn	Asp	Ile	Leu	Leu	Gly	Glu	Ala	Arg	Arg	Ser	Ser	Gly		

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Asp Ala Ser Val Arg Phe Ala Val Ser Lys Ser Val Asp Glu Val Arg
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Gly Thr Asp Thr Pro Pro Glu Lys Val Pro Arg Arg Val Leu Pro Ser
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Gly Phe Lys Pro Ala Glu Ser Ala Gly Asp Ala Ser Ser Leu Phe Ser
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Asn Ile Met His Lys Phe Val Lys Val Asp Asp Arg Asp Cys Ser Gly
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Glu Arg Ser Arg Glu Asp Val Val Pro Leu Asn Asp Ser Ser Leu Cys
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Met Lys Ala Asn Asp Val Ile Pro Gln Phe Arg Ser Asn Asn Gly Lys
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Thr Gln Glu Arg Asn His Ala Phe Ser Phe Ser Gly Arg Ala Glu Leu
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Arg Ser Val Glu Asp Ile Gly Val Asp Gly Asp Val Pro Gly Pro Glu
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Thr Pro Gly Met Arg Pro Arg Ala Ser Arg Leu Lys Arg Val Leu Glu
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Asp Glu Met Thr Phe Lys Glu Asp Lys Val Pro Val Leu Asp Ser Asn

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Asp	Ala	Asn	Arg	Arg	Arg	Pro	Asp	Asp	Pro	Leu	Tyr	Asp	Arg	Lys	Thr
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Leu	His	Ile	Pro	Pro	Asp	Val	Phe	Lys	Lys	Met	Ser	Ala	Ser	Gln	Lys
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Gln	Lys	Cys	Ser	Thr	Val	Tyr	Gly	Phe	Ala	Phe	Val	Asp	Cys	Ala	Ala
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Gly	Asp	Thr	Asp	Ala	Ala	Gly	Val	Arg	Asn	Ile	Ile	Glu	Ser	Asn	Gly
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Tyr	Phe	Lys	Gly	Ser	Ser	Glu	Ser	Trp	Asn	Cys	Ala	Val	Asp	Gly	Leu
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Asn	Glu	Cys	Asp	Val	Ala	Leu	Ser	Ala	Leu	Gly	Glu	Leu	Ile	Asn	His
	515					520						525			

Leu	Ser	Arg	Leu	Lys	Leu	Glu	Asp	Val	Leu	Lys	His	Gly	Asp	Ile	Phe	530	535	540
Pro	Tyr	Gln	Val	Tyr	Arg	Gly	Cys	Leu	Arg	Ile	Asp	Gly	Gln	Thr	Met	545	550	555
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Thr	Leu	Tyr	Lys	Tyr	Leu	Asp	Asn	Cys	Val	Ser	Pro	Thr	Gly	Lys	Arg	580	585	590
Leu	Leu	Arg	Asn	Trp	Ile	Cys	His	Pro	Leu	Lys	Asp	Val	Glu	Ser	Ile	595	600	605
Asn	Lys	Arg	Leu	Asp	Val	Val	Glu	Glu	Phe	Thr	Ala	Asn	Ser	Glu	Ser	610	615	620
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Pro	Ala	Leu	Leu	Gly	Lys	Lys	Val	Leu	Lys	Gln	Arg	Val	Lys	Ala	Phe	660	665	670
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Phe	Glu	Ala	Ala	Ile	Asp	Ser	Asp	Phe	Pro	Asn	Tyr	Gln	Asn	Gln	Asp	725	730	735
Val	Thr	Asp	Glu	Asn	Ala	Glu	Thr	Leu	Thr	Ile	Leu	Ile	Glu	Leu	Phe	740	745	750
Ile	Glu	Arg	Ala	Thr	Gln	Trp	Ser	Glu	Val	Ile	His	Thr	Ile	Ser	Cys	755	760	765
Leu	Asp	Val	Leu	Arg	Ser	Phe	Ala	Ile	Ala	Ala	Ser	Leu	Ser	Ala	Gly	770	775	780
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Pro	Phe	Ala	Val	Ala	Ala	Asp	Gly	Gln	Leu	Pro	Val	Pro	Asn	Asp	Ile	820	825	830
Leu	Leu	Gly	Glu	Ala	Arg	Arg	Ser	Ser	Gly	Ser	Ile	His	Pro	Arg	Ser	835	840	845

Leu Leu Leu Thr Gly Pro Asn Met Gly Gly Lys Ser Thr Leu Leu Arg
 850 855 860
 Ala Thr Cys Leu Ala Val Ile Phe Ala Gln Leu Gly Cys Tyr Val Pro
 865 870 875 880
 Cys Glu Ser Cys Glu Ile Ser Leu Val Asp Thr Ile Phe Thr Arg Leu
 885 890 895
 Gly Ala Ser Asp Arg Ile Met Thr Gly Glu Ser Thr Phe Leu Val Glu
 900 905 910
 Cys Thr Glu Thr Ala Ser Val Leu Gln Asn Ala Thr Gln Asp Ser Leu
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 Val Ile Leu Asp Glu Leu Gly Arg Gly Thr Ser Thr Phe Asp Gly Tyr
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 Ala Ile Ala Tyr Ser Val Phe Arg His Leu Val Glu Lys Val Gln Cys
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 Arg Met Leu Phe Ala Thr His Tyr His Pro Leu Thr Lys Glu Phe Ala
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 Ser His Pro Arg Val Thr Ser Lys His Met Ala Cys Ala Phe Lys Ser
 980 985 990
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<220>
 <223> Forward primer for PCR amplification of ATHGENEA
 microsatellite

<400> 32

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<210> 33

<211> 22

<212> DNA

<213> Artificial sequence

<220>

<223> Reverse primer for PCR amplification of ATHGENEA
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<400> 33

acataaccac aaataggggt gc 22

<210> 34

<211> 18

<212> DNA

<213> Artificial sequence

<220>

<223> Forward primer DMCIN-A for PCR on genomic DNA of Arabidopsis
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ssp. Landsberg erecta "Ler"

<400> 34

gaagcgatat tgttcgtg 18

<210> 35

<211> 18

<212> DNA

<213> Artificial sequence

<220>

<223> Reverse primer DMCIN-B for PCR on genomic DNA of Arabidopsis
thaliana
ssp. Landsberg erecta "Ler"

<400> 35

agattgcgag aacattcc 18

<210> 36

<211> 31

<212> DNA

<213> Artificial sequence

<220>

<223> Forward primer DMCIN-1 for PCR on genomic DNA of Arabidopsis
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ssp. Landsberg erecta "Ler"

<400> 36

acgcgtcgac tcagctatga gattactcgt g 31

<210> 37
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ssp. *Landsberg erecta* "Ler"

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<210> 38
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ssp. *Landsberg erecta* "Ler"

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<210> 39
<211> 48
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<220>
<223> Reverse primer DMCIN-4 for PCR on genomic DNA of *Arabidopsis thaliana*
ssp. *Landsberg erecta* "Ler"

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<210> 40
<211> 26
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<223> Forward primer DMC1a for PCR on genomic DNA of *Arabidopsis thaliana* ssp.
Landsberg erecta "Ler"

<400> 40
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<210> 41
<211> 38
<212> DNA
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gccactgcgt gaatgatatg 20

<210> 43
<211> 22
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<220>
<223> Reverse primer for PCR amplification of ATEAT1 SSLP marker in *Arabidopsis thaliana* subspecies

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cgaacagcca acattaattc cc 22

<210> 44
<211> 18
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aaccaaggca cagaagcg 18

<210> 45

<211> 18
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Arabidopsis
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Arabidopsis thaliana subspecies

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<210> 50
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ccttcacatc caaaaccac 20

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<210> 63

<211> 22

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<223> Reverse primer for PCR amplification of AthBIO2 SSLP marker in Arabidopsis thaliana subspecies

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<210> 64

<211> 21

<212> DNA

<213> Artificial sequence

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<223> Forward primer for PCR amplification of AthUBIQUE SSLP marker in Arabidopsis thaliana subspecies

<400> 64

aggcaaattgt ccatttcatt g 21

<210> 65

<211> 20

<212> DNA

<213> Artificial sequence

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<223> Reverse primer for PCR amplification of AthUBIQUE SSLP marker in Arabidopsis thaliana subspecies

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acgacatggc agatttctcc 20

<210> 66

<211> 21

<212> DNA

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<223> Forward primer for PCR amplification of NGA172 SSLP marker in Arabidopsis thaliana subspecies

<400> 66
 agctgcttcc ttatagcgtc c 21

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 Arabidopsis thaliana subspecies

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 Arabidopsis thaliana subspecies

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 caagagcaat atcaagagca gc 22

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 thaliana subspecies

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 Arabidopsis thaliana subspecies

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<400> 79

cgacgaatcg acagaattag g 21

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gaaatccaaa tcccagagag g 21

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<400> 82

taccgtcaat ttcacgccc 19

<210> 83
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<210> 84

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<223> Forward primer for PCR amplification of CA72 SSLP marker in
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<400> 84

aatcccagta accaaacaca ca 22

<210> 85

<211> 20

<212> DNA

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<223> Reverse primer for PCR amplification of CA72 SSLP marker in
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thaliana subspecies

<400> 85

cccagtctaa ccacgaccac 20

<210> 86

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<223> Forward primer for PCR amplification of NGA151 SSLP marker in
Arabidopsis thaliana subspecies

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<223> Reverse primer for PCR amplification of NGA151 SSLP marker in
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<210> 89
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 in
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 ctccaccaat catgcaaag 20
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<223> Forward primer for PCR amplification of NGA129 SSLP marker in
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<400> 98

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